

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 5, 2003, 04:01:18 ; Search time 122 Seconds
(without alignments)

3163.556 Million cell updates/sec

Title: US-09-847-081B-2

Perfect score: 2270

Sequence: 1 MSMSVALLWVSTPVSNG.....IYAKSLVPPNRTSPLAKT 440

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186958

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 10%

Listing first 45 summaries

Command line parameters:

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-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PublishedApplications_NA:

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2270	100.0	1728	10	US-09-847-081B-1
2	1801	79.3	1712	10	US-09-847-081B-3
3	1737	76.5	1239	10	US-09-371-307-75
4	1542	67.9	1269	9	US-09-938-842A-729

5	350.5	15.4	1232	12	US-10-041-472-1	Sequence 1, Appli
6	336.5	14.8	891	9	US-09-941-947A-33	Sequence 33, Appl
c 7	326	14.4	8625	9	US-09-920-923-1	Sequence 1, Appli
c 8	326	14.4	11233	9	US-09-920-923-27	Sequence 27, Appl
9	324	14.3	908	10	US-09-547-267-4	Sequence 4, Appli
10	306	13.5	1020	9	US-09-918-740-71	Sequence 71, Appl
11	306	13.5	7252	9	US-09-918-740-73	Sequence 73, Appl
12	306	13.5	7252	9	US-09-918-740-75	Sequence 75, Appl
c 13	293	12.9	536165	9	US-09-939-964-1	Sequence 1, Appli
14	273.5	12.0	2174	7	US-08-781-986A-202	Sequence 202, App
15	204	9.0	912	9	US-09-738-626-695	Sequence 695, App
c 16	202.5	8.9	3309400	9	US-09-738-626-1	Sequence 1, Appli
17	198	8.7	876	9	US-09-738-626-2673	Sequence 2673, Ap
18	113	5.0	1242	9	US-09-938-842A-50	Sequence 50, Appl
19	112.5	5.0	114	9	US-10-103-450-12	Sequence 12, Appl
20	112.5	5.0	114	9	US-10-137-765-9	Sequence 9, Appli
21	112.5	5.0	114	9	US-10-146-337-9	Sequence 9, Appli
22	111.5	4.9	1606	10	US-09-820-004-1	Sequence 1, Appli
23	109.5	4.8	1662	10	US-09-917-800A-1669	Sequence 1669, Ap
24	109	4.8	17581	9	US-10-091-504-2170	Sequence 2170, Ap
25	109	4.8	17581	10	US-09-764-869-2170	Sequence 2170, Ap
26	109	4.8	40090	10	US-09-820-004-3	Sequence 3, Appli
c 27	103.5	4.6	1168	10	US-09-770-445-56	Sequence 56, Appl
c 28	103.5	4.6	13856	7	US-09-781-986A-31	Sequence 31, Appl
29	103	4.5	6613	12	US-10-032-717-28	Sequence 28, Appl
30	101	4.4	514	9	US-09-940-244-287	Sequence 287, App
31	101	4.4	1023	9	US-10-033-297-78	Sequence 78, Appl
32	101	4.4	1023	9	US-09-940-244-78	Sequence 78, Appl
33	101	4.4	1115	9	US-09-940-244-289	Sequence 289, App
34	101	4.4	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 35	100.5	4.4	533	10	US-09-998-598-2126	Sequence 2126, Ap
c 36	99	4.4	19695	10	US-09-826-191-3	Sequence 3, Appli
c 37	97.5	4.3	1050	9	US-09-738-626-530	Sequence 530, App
38	97	4.3	996	9	US-09-938-842A-1379	Sequence 1379, Ap
c 39	96.5	4.3	48908	9	US-10-114-170-137	Sequence 137, App
c 40	95.5	4.2	30365	10	US-09-825-414-1	Sequence 1, Appli
41	94.5	4.2	1518	9	US-10-116-821-13	Sequence 13, Appl
42	94	4.1	1536	10	US-09-912-020-99	Sequence 99, Appl
43	93	4.1	1512	10	US-09-815-242-6983	Sequence 6983, Ap
44	92.5	4.1	2887	10	US-09-925-297-242	Sequence 242, App
c 45	92	4.1	1929	10	US-09-826-660-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-847-081B-1
; Sequence 1, Application US/09847081B
; Patent No. US20020128464A1
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
; FILE REFERENCE: Le 34 326
; CURRENT APPLICATION NUMBER: US/09/847.081B
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (244)..(1566)
US-09-847-081B-1

Alignment Scores:
Pred. No.: 2,47e-272 Length: 1728
Score: 2270.00 Matches: 440
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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US-09-847-081B-2 (1-440) x US-09-847-081B-3 (1-1712)

Qy      3 MetSerValAlaLeuLeuTyrValValSerProThrSerGluValSerAsnGlyThrGly  22
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      333 ATGTCGTTGCCCTGTATGGGTGTTTCACCT---TGTGAAGTCTCAAAATGGGCACAGA  389
      |||
Qy      23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg  42
      |||
      390 TTCCTGGATTACGTCGCGGAGGGAACCGGGTTTGTGATTCGTCG-----AGG  437
      |||
Qy      43 AspArgAsnLeuMetTyrAsnGlyArgIleLysLysGlyGlyArgGlnArgTrpAsnPhe  62
      |||
      438 CATAGGAATTTAGTGTGCCAATGNAGAAACACAGAGAGGTGCTGAACAAGGTGGNAATTT  497
      |||
Qy      63 GlySerLeuIleAlaaspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly  82
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      498 GGT-----  500

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Db	469	TCGAGAAGAACAGATGAACCTTGTGATGGCCCAACGCATCATATATACCCGGCAGCC	528
QY	203	LeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu	222
Db	529	CTAGATAGCTGGGAAATAGGCTAGAACATCTTTTCAATGGCGGCCCATTTGACATGCTC	598
QY	223	AspAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp	242
Db	589	GATGGTGGCTTTTCCGATACAGTTTCTAACTTCCAGTTGATATTCAGCCATTCAGAGAT	648
QY	243	MetIleGluGlyMetArgMetAspLeuThrPlySerArgTrpLysThrPheAspGluLeu	262
Db	649	ATGATTGAAGGAATCGGTATGGACTTGAGAAATCGAGATACAAAACTTCGACGAACTA	708
QY	263	TyrLeuTrpCysTrpTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly	282
Db	709	TACCTTTATTGTATTATGTGCTGCTACGCTGGGTGGTTGATGAGTTCCTCAATTATGGGT	768
QY	283	IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaLeuAlaLeuGly	302
Db	769	ATCGCCCTCGAATCAAGGCACACAGAGAGCGGTATATAATGCTGCTTTGGCTCTGGGG	828
QY	303	LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArg	322
Db	829	ATCGCAAAATCAATTAACTAACATATCTAGAGATGTGGGAGAGATGCCAAGAGGAAGA	888
QY	323	ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAla	342
Db	889	GTCTACTTGCCTCAGATGAATTACACAGCCAGGCTCTATCCGATGAAGATATATTGCT	948
QY	343	GlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLys	362
Db	949	GGAAAGGTGACCGATAAATGGAGATCTTTATGAAGAACAAATACATAGSGCAAGAAG	1008
QY	363	PhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpProVal	382
Db	1009	TTCTTTTGATGGCGCAGAGAAATGGCGTGACAGAAATTGAGCTCAGCTAGTATATCCCTGTA	1068
QY	383	LeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsn	402
Db	1069	TGGGCATCTTTGGTCTTGACCGCAAAATACTAGATGAGATTGAAGCCAAATGACTACAC	1128
QY	403	AsnPheThrArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIleAla	422
Db	1129	AACTTCACAAAGAGAGACATATGTGACCAAAATCAAGAAAGTTGATTCGATTACCTATTGCA	1188
QY	423	TyrAlaLysSerLeuValProProAsnArgThrSerSer	435
Db	1189	TATGCAAAATCTTTGTGCTCTCTACAAAACTGCCTCT	1227

QY 295 rsnAlaLaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValG1 315
Db 840 CAACGCTGCTGGCCCTGGTATAGCCAATCAGCTTACTACATCTACAGAGCTAGG 899
QY 315 YGluAspAlaArgGlyValGlyValLeuProGlnAspGluLeuAlaGlnAlaGlyLe 335
Db 900 CGAAGATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959
QY 335 uSerAspGluAspIlePheAlaGlyArgValThrAspLysTyrArgAsnPheMetLysLy 355
Db 960 TTCAGATGAGACATATTCGCGGGAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 1019
QY 355 scInleGlnArgAlaArgLysPheAspGluSerGluLysGlyValThrGluLeuAs 375
Db 1020 CGAGCTTAACGAGCAAGAAATCTTCGACGAGCTGAGAAAGCGTCACCGAGCTCAG 1079
QY 375 pSerAlaSerArgTppProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspG1 395
Db 1080 TCCCGCTGACAGATGGCTGTATGGCTTCATGTGTATGTACAGGAGAAATACTGGACGA 1139
QY 395 ulleGluAlaAsnAspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLy 415
Db 1140 GATTGAAGCGAATGATTACACAAATTTTACTAAGAGAGCTTATGTGGGAAAGTCAAGAA 1199
QY 415 sleuLeuThrLeuProIleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSe 435
Db 1200 AATTCAGCTTGCCATTGGCTTATGCTTAAATCAGTACTA-----AAGACTTCAAG 1250
QY 435 x 435
Db 1251 T 1251

RESULT 5

US-10-041-472-1
; Sequence 1, Application US/10041472
; Patent No. US20020092039A1
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, Christine
; TITLE OF INVENTION: METHODS FOR PRODUCING CAROTENOID COMPOUNDS AND SPECIALITY OILS IN
; FILE REFERENCE: 16516.141
; CURRENT APPLICATION NUMBER: US/10/041.472
; CURRENT FILING DATE: 2002-01-10
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: US 08/908758
; PRIOR FILING DATE: 1996-09-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Erwinia uredovora
US-10-041-472-1

Alignment Scores:

Pred. No.: 9.4e-34 Length: 1232
Score: 350.50 Matches: 110
Percent Similarity: 43.88% Conservative: 55
Best Local Similarity: 29.26% Mismatches: 162
Query Match: 15.44% Indels: 49
Db: 12 Gaps: 11

US-09-847-081B-2 (1-440) x US-10-041-472-1 (1-1232)

QY 77 SerArgThrGluLysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAla 96
Db 83 AGCCGTGCTCTAGAGGGG-----CAATCCGCGCAGTGGCTCCATTCGCGC 127
QY 97 Gly-----GluMetThrValSerSerGluLysLysValTyrAspValValLeuLysGln 114
Db 128 GGCCCTCAATCCATGCTGGATTCCCATGAGAGAGGTC----- 166

QY 115 AlaAlaLeuValLysArgGlnLeuArgSerThrAspLeuGluValLysProAsp--- 133
Db 167 -----AACACTGACATTACTTCCATTACAAACAATGGT 199
QY 134 -----IleValValProGlyAsnLeuGlyLeuLeuSerGluAlaTyrAspArgCysGly 151
Db 200 GGAAGAGTAAAGTGCATGAATATCCGCTGTACTCAATCATCGCGTC----- 247
QY 152 GluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGlu 171
Db 248 GAACAGATGGCGTAGTGGCTCGAAAGATTTCGACAGCCTCAAGATTATTGTGATGACAA 307
QY 172 ArgArgArgAlaIleTyrValTyrPheTyrCysArgArgThrAspGluLeuValAsp 191
Db 308 ACCCGCGCAGCGTACTGATGCTTACGCTGGTGGCGCATGTGACGATGTATTGATGAC 367
QY 192 GlyProAsn-----AlaSerHisIleThrProGlnAlaLeu 203
Db 368 GATCAGACGCTGGGCTTTTCAGGCGCGGCGACCTGCCTTACAAACGCCCAACACGCTCG 427
QY 204 AspArgTyrGluThrArgLeuGluAspIlePheSerGly---ArgProPheAspMetLeu 222
Db 428 ATGCAACTTGAATGAAACAGCGCGCATGATGAGGATCGCAGATGCGAAGCAGCGCGG 487
QY 223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg--- 241
Db 488 TTTGCGGCTTTTCAGGAAGTGGCTATGGCTCAT-----GATATCCCGCGGCTTACGCG 541
QY 242 ---AspMetIleGluGlyMetArgMetAspLeuTyrLysSerArgTyrLysThrPheAsp 260
Db 542 TTTGATCATCTGGAAGGCTTCGCCATGGATGTACGGAAGCGCAATACAGCAACTGGAT 601
QY 261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
Db 602 GATACGCTGGCTATGTATGCTATGCGTGGCGGCTGTGCGGTGTGATGATGGCGCAAT 651
QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300
Db 662 ATGGCGGT-----CGGGATAACGCCACGCTGGAC-----CGCGGCTGTGAC 703
QY 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
Db 704 CTGGGCTGGCATTTTCAGTTGACCAATATTGCTCGCATATTGTGCGCATGCGCATGCG 763
QY 321 GlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340
Db 764 GGCCGCTGTATCTCGCGCAAGCTGGCTGGAGCATGAAGGCTGAACAAAGAGATTAT 823
QY 341 PheAlaGlyArgValThrAspLysTyrArgAsnPheMetLysLysGlnIleGlnArgAla 360
Db 824 GCGGCACCTGAAACCGCTCAGCGCTGAGCCGCTATCGCCGCTGTTGGTGCAAGAGCA 883
QY 361 ArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTyr 380
Db 884 GAACCTTACTATTGCTGTCACAGCGCGCTGGCAGGCTTGCCTTGGCTTCCGCTGG 943
QY 381 ProValLeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAsp 400
Db 944 GCAATCGCTACGGCGAAGCAGGTTTACCGGAAATATGTTGTTGTTGTTGTTGTTGTT 1003
QY 401 TyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuPro 420
Db 1004 CAGCAAGCCTGGGATCAGCGGCGAGTCAACGACCCCGCGGAAATTAACGCTGCTGCTG 1063
QY 421 IleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerPro 436
Db 1064 GCCGCTCTGTGTCAGCGGCTTACTCCCGGATGCGGCTCATCTCTCCC 1111

RESULT 6

US-09-941-947A-33
; Sequence 33, Application US/09941947A
; Publication No. US20030003528A1

```

; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qiong
; APPLICANT: DiCosimo, Deana J.
; APPLICANT: Koffas, Mattheos
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odom, J. Martin
; APPLICANT: Picastaggio, Steve
; APPLICANT: Rouvere, Pierre E.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CL1903 US NA
; CURRENT APPLICATION NUMBER: US/09/941-947A
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Pantoea stewartii
; US-09-941-947A-33

Alignment Scores:
Pred. No.: 3,15e-32 Length: 891
Score: 336.50 Matches: 88
Percent Similarity: 48.28% Conservative: 52
Best Local Similarity: 30.34% Mismatches: 131
Query Match: 14.8% Indels: 19
DB: 6 Gaps: 6

US-09-847-081B-2 (1-440) x US-09-941-947A-33 (1-891)
QY 158 AlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTTP 177
DB 13 TCGAAAGCTTTCGACTGATCGAGCGCTTCGAGCGCCAAACCCGTCGACGGTGTG 72
QY 178 AlaIleTyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsn----- 194
DB 73 ATGCTTTACGCATGGTGGCCGACATCGAGCGAGTCAATGACGATCAACACACTGGGCTTT 132
QY 195 -----AlaSerHisIleThrProGluAlaLeuAspArgTrpGluThrArg 209
DB 133 CATGCGACGACGCCCTTCGCGAGATGCTGAGCAGCGCTTCGAGCGTTCGAAATGAAA 192
QY 210 LeuGluAspIlePheSerGly---ArgProPheAspMetLeuAspAlaLeuSerAsp 228
DB 193 ACAGCTCAGCGCTACCGCGTTCGAAATGACGACGCGCTTCGCGGTTTCAGGAG 252
QY 229 ThrValSerArgPheProValAspIleGlnProPheArg-----AspMetIleGluGly 246
DB 253 GTGCGCATGGCGCAT-----GATATCGCTCCGCGCTACGCGTTCGACCATCTGGAAGT 306
QY 247 MetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrIleTyrCys 266
DB 307 TTGCGCATGATGTCGCGAAGCGCTACCTGACACTGGAGCATACGCTGGCTTATTCG 366
QY 267 TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGlu 286
DB 367 TATCAGCTCGCGGTGTTGGGCGCTGATGATGGCCCAATATATGGCGTT-----CGC 420
QY 287 SerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGln 306
DB 421 GATAAGCCACGCTCAT-----CGCGCTGGCATCTCGGCTGGCTTTCCAG 468
QY 307 LeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArgValTyrLeuPro 326
DB 469 TTGACCAACATTCGCGGTGATATGTCGAGATGCTCAGGTGGCGCTGTTATCTGCCT 528
QY 327 GlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThr 346
DB 4286 -----GCCATCGCGAGGGTTTCGCAAGCTTCGCGCAGCGCGCAAGTATCGCCGCC 4233

; Sequence 1, Application US/09920923
; Publication No. US2003002273A1
; GENERAL INFORMATION:
; APPLICANT: Tszygankov, Yuri
; APPLICANT: Pasamontes, Luis
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/09/920,923
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8625
; TYPE: DNA
; ORGANISM: Flavobacterium sp. R1534
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8348)..(8349)
; NAME/KEY: unsure
; LOCATION: (8539)..(8540)
; NAME/KEY: unsure
; LOCATION: (8581)
; NAME/KEY: unsure
; LOCATION: (8590)
; NAME/KEY: unsure
; LOCATION: (8592)
; NAME/KEY: unsure
; LOCATION: (8602)..(8604)
; US-09-920-923-1

Alignment Scores:
Pred. No.: 2,12e-29 Length: 8625
Score: 326.00 Matches: 102
Percent Similarity: 47.18% Conservative: 40
Best Local Similarity: 33.89% Mismatches: 117
Query Match: 14.36% Indels: 42
DB: 9 Gaps: 12

US-09-847-081B-2 (1-440) x US-09-920-923-1 (1-8625)
QY 135 ValValProGly-----AsnLeuGlyLeuLeuSerGluAlaTyrAspArgCys 150
DB 4334 GTCGACCGTGGCGCTGCGATGACCGCATCTGACGCGGACTTCGGAAGCG----- 4287
QY 151 GlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrPro 170
DB 4286 -----GCCATCGCGAGGGTTTCGCAAGCTTCGCGCAGCGCGCAAGTATCGCCGCC 4233

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QY 396 IleGluAlaAsnAspTyrAsnAsnPhetThrArgArgAlaTyrValSerLysProLysLys 415
 Db 4245 ATCCGACGGTGGCCCGCAGGCTATCCGACGGGATCAGCAGCTCGAAGGCTGCCAAG 4186
 QY 416 Leu 416
 Db 4185 ATC 4183

RESULT 9

US-09-547-267-4
 ; Sequence 4, Application US/09547267
 ; Patent No. US20020147371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hohmann, Hans-Peter
 ; APPLICANT: Pasamontes, Luis
 ; APPLICANT: Tessier, Michel
 ; APPLICANT: van Loon, Adolphus
 ; TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingsland Street
 ; CITY: Nutley
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/547,267
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/660,645
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pokras, Bruce A.
 ; REGISTRATION NUMBER: 32,748
 ; REFERENCE/DOCKET NUMBER: RAN 6002/170
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (201) 235-5801
 ; TELEFAX: (201) 235-2363
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 908 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-547-267-4

Alignment Scores:
 Pred. No.: 1.16e-30 Length: 908
 Score: 324.00 Matches: 95
 Percent Similarity: 48.3% Conservatives: 39
 Best Local Similarity: 34.30% Mismatches: 111
 Query Match: 14.27% Indels: 32
 DB: 10 Gaps: 10

US-09-847-081B-2 (1-440) x US-09-547-267-4 (1-908)

QY 155 AlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 174
 Db 37 GCGCAGGGTTCGAAGCTTCGCGAGGGCGCAAGCTGATCCGCGCGCATCCGCGAG 96
 QY 175 AlaIleTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 192
 Db 97 GATACGGTATCTATCCCTGGTGCAGGATCGGATGACGTGATCGACGGCAGGTG 156
 QY 193 -----ProAsnAlaSerHisIleThrProGlnAla----- 202

Db 157 ATGGGTTCGCCCGAGCGCGCGGC-----GACCCACAGCGCGGTGGGGCGCTCGCG 213
 QY 203 LeuAspArgTyrPgluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222
 Db 214 GCGCAGCGCTGCGCGCGTGCACGAGGACGCCGATGTCGCCGCCCTTC----- 264
 QY 223 AspAlaAlaLeuSerAspThrValSerArg-----PheProValAspIleGlnProPhe 240
 Db 265 ---GCGGGCGCTCGCCAGGTGCGCGCGCGCATGATTCCCG---CACCTTTGCCCGCATG 318
 QY 241 ArgAspMetIleGluGlyMetArgMetAspLeuTyrPheSerArgTyrLysThrPheAsp 260
 Db 319 ---GACCTGATCGAGGGTTTCGCGATGATGTCGCGGATCGCGAATACCGACCTGGAT 375
 QY 261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
 Db 376 GACGTGCTGGAATATCTACACAGTTCGCGGGGGTCTGGCGGTGATGATGGCGCGGGTG 435
 QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300
 Db 436 ATGGCGGTG-----CAGGACGATGCGGTGCTGCTGATCGCGCTCGCAT 477
 QY 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
 Db 478 CTGGGCGCTTGGCTTCAGCTGACGAACATCGCTCGCGAGCTGATCGACATCGCGCATC 537
 QY 321 GlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340
 Db 538 GGGCGCTGCTATCTGCTGCCACTGCTGGTGGCGGAGCGGGCGGAGGTTGAG----- 591
 QY 341 PheAlaGlyArgVal---ThrAspLysTyrArgAsnPhetMetLysLysGlnIleGlnArg 359
 Db 592 -----GGTCCGCTGCTTCGCGACGCGCTCTATTTCGTGTCATCATCGCGCTGCTGACGCG 645
 QY 360 AlaArgLysPheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArg 379
 Db 646 GCGGAGCGCTATATGCTCGCGGCGGAGGGCTTCGCGCATCTGCGCGCGCGCTCGCGG 705
 QY 380 TrpProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsn 399
 Db 706 TGGTCGATCGCGCGCGCTGCTGCTATCTATCGCAATCGGACGCGCATCGCGCAGGCT 765
 QY 400 AspTyrAsnAsnPhetThrArgArgAlaTyrValSerLysProLysLysLeu 416
 Db 766 GCGCCCGAGGCGCTATCGCGACGCGGATCAGCAGCTCGAAGGCTGCCAAGATC 816

RESULT 10

US-09-918-740-71
 ; Sequence 71, Application US/09918740
 ; Publication No. US20030033626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hahn, Frederick
 ; APPLICANT: Kuehnle, Adelheid
 ; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathway
 ; FILE REFERENCE: KAS-103XCI
 ; CURRENT APPLICATION NUMBER: US/09/918,740
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/221,703
 ; PRIOR FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: Patent In version 3.0
 ; SEQ ID NO 71
 ; LENGTH: 1020
 ; TYPE: DNA
 ; ORGANISM: Rhodobacter capsulatus
 ; US-09-918-740-71

Alignment Scores:
 Pred. No.: 2.41e-28 Length: 1020
 Score: 306.00 Matches: 90
 Percent Similarity: 48.79% Conservatives: 51

QY 365 AspGluSerGluYsGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThr 384
 Db 4782 TGGCGGGCGGCGAGGGGGTGGGCTTTTGGCTTGGCTGCGCGGGGATCGGCC 4841
 QY 385 AlaLeuLeuYsArgGlyLysLeuAspGluLeuGluAlaAsnAspTrpAsnAsn 404
 Db 4842 GCGGCAAGATCTATGCGCGATCGGGCGGAGTGGCGAAGCGGAATACGACATC 4901
 QY 405 ThrArgAlaValSerLysLysLeuLeuThrLeuPro 420
 Db 4902 ACCCGCGTGGCCACACGACCAAGGCGCGAAGCTGTGGCTGGTGGCGAATCCGCGATG 4961
 QY 421 IleAlaValAlaLysSerLeuValPro 429
 Db 4962 TCGGCGACGCGACCTCGATGTCGCG 4988

RESULT 12

US-09-918-740-75
 ; Sequence 75, Application US/09918740
 ; Publication No. US20030033826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hahn, Frederick
 ; APPLICANT: Kuehnle, Adelheid
 ; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways
 ; FILE REFERENCE: KAS-103XCI
 ; CURRENT APPLICATION NUMBER: US/09/918,740
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: 60/221,703
 ; PRIOR FILING DATE: 2000-07-31
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 75
 ; LENGTH: 7252
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (..)(..)
 ; OTHER INFORMATION: Plasmid transformation vector pPHO5 containing R. capsulatus DNA
 ; OTHER INFORMATION: e
 US-09-918-740-75.

Alignment Scores:

Pred. No.:	4,98e-27	Length:	7252
Score:	306.00	Matches:	90
Percent Similarity:	48.79%	Conservative:	51
Best Local Similarity:	31.14%	Mismatches:	130
Query Match:	13.48%	Indels:	18
DB:	9	Gaps:	6

US-09-847-081B-2 (1-440) x US-09-918-740-75 (1-7252)

QY 152 GluValCysAlaGluValThrAlaLysThr-----PheTyrLeuGlyThrLysLeu 167
 Db 4143 GAGGTCTGCGGGAGTGTATCGCCAGCGAGCTACTCTTCATCGCGGTCACAGTT 4202
 QY 168 MetThrProGluArgArgAlaLysThrAlaLysValThrCysArgArgThrAsp 187
 Db 4203 CTGCGGCGGGTCTGCGTACCGCGCTGGCGCTTTTACGCTTTTGGCGGTCGCGAT 4262
 QY 188 GluLeuValAspGlyProAsnAlaSerHisLeuThrProGlnAlaLeuAspArgTrpGlu 207
 Db 4263 GACGAAGTCGACAGGTGTGGCGCGCGCGAGCAAGGCTGCGCGGTGTTGAACCTTGGC 4322
 QY 208 ThrArgLeuGluAspPheSerGlyArgProPheAspMet---LeuAspAlaLeu 226
 Db 4323 GACCGGTGGAGGACATCTATGCGGTGTCGCGGCAATGCGGCTCGGATCGGGCTTTC 4382
 QY 227 SerAspThrValSerArgPheProValAspPheGlnProPheArgAspMetIleGluGly 246
 Db 4383 GCGGCGGTGTCGAGGAAATCGAGATGCGCGCGAATTCGCCGAGCGGTGCTGGAGGCG 4442

QY 247 MetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCys 266
 Db 4443 TTCGCTGCTGCGAGCGGGGGTGGTATCACACGCTTTCGACGCTGCGAGGCTATTCG 4502
 QY 267 TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAla---Pro 285
 Db 4503 GCGCGGGTGGCGCGCGCTGCGCGGATGATGTGGCTGCTGATCGGTCGCGACACCC 4562
 QY 286 GluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsn 305
 Db 4563 GATGCTGCGC-----CGGCGCTGCGATCTCGGTCTTGCATG 4601
 QY 306 GlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArgValLeu 325
 Db 4602 CAGATGTGCAACATCGCCGCGACGCTGGCGGAGGATGCCCGGCGGGGCTTTCTCTG 4661
 QY 326 ProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGly---Arg 344
 Db 4662 CCGACCGACTGATGTCGAGGAGGGATCGATCCCGAGCGTTCCTGCCGATCGCAG 4721
 QY 345 ValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePhe 364
 Db 4722 CCACCAAGGGCATCGCGCGGTTCACCGAGCGTTCCTGAACCGCGCGCGCTTAC 4781
 QY 365 AspGluSerGluYsGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThr 384
 Db 4782 TGGCGGCGCGCGCGGGGTGGGCTTTTGGCTTTGCTGCTGCGCGCGGGGATCGGCG 4841
 QY 385 AlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsnAsn 404
 Db 4842 GCGGCAAGATCTATCGCGGATCGGGCGGAGTGGCGAAGCGGAATACGACATC 4901
 QY 405 ThrArgAlaValSerLysLysLysLysLysLysLysLysLysLysLysLysLysLys 420
 Db 4902 ACCCGCGTGGCCACACGACCAAGGCGCGAAGCTGTGGCTGGTGGCGAATTCGCGATG 4961
 QY 421 IleAlaValAlaLysSerLeuValPro 429
 Db 4962 TCGGCGACGCGACCTCGATGTCGCG 4988

RESULT 13

US-09-939-964-1/c
 ; Sequence 1, Application US/09939964
 ; Publication No. US20030054522A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosenthal, Andre
 ; APPLICANT: Freiberg, Christoph
 ; APPLICANT: Perret, Xavier Philippe
 ; APPLICANT: Broughton, William John
 ; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
 ; FILE REFERENCE: CARP0068
 ; CURRENT APPLICATION NUMBER: US/09/939,964
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: 09/214,808
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 536165
 ; TYPE: DNA
 ; ORGANISM: Rhizobium
 US-09-939-964-1

Alignment Scores:

Pred. No.:	1,58e-22	Length:	536165
Score:	233.00 <td>Matches: <td>95 </td></td>	Matches: <td>95 </td>	95
Percent Similarity:	46.75% <td>Conservative:</td> <td>49 </td>	Conservative:	49
Best Local Similarity:	30.84% <td>Mismatches:</td> <td>112 </td>	Mismatches:	112
Query Match:	12.91% <td>Indels:</td> <td>52 </td>	Indels:	52
DB:	9 <td>Gaps:</td> <td>11 </td>	Gaps:	11

QY 273 ValGlyLeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGlu 292
 Db 1750 GTAGGTGAAGTATTGACGGCGATTTA-----AGTATCATGAACACAT 1794
 QY 293 SerValTyrAsnAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArg 312
 Db 1795 CAGACATACGATGTCGCAAGAGACTGCTGAATCGTTCAATTGATTATATAAAGA 1854
 QY 313 AspValGlyGluAspAlaArgGlyArgValTyrLeuProGlnAspGluLeuAlaGln 332
 Db 1855 GATGTCGGTGAAGATTTTGCACATGACGATATATTTAGTAAGCAACGATTAAGCAA 1914
 QY 333 AlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTyrArgAsnPhe 352
 Db 1915 TATGAAGTTGATTTCTGACGTACCAAAATGGTTTAATAATCATTTATGACTTA 1974
 QY 353 MetLysLysGlnIleGlnArgAlaArgLysPhePheAspGluSerGluLysGlyValThr 372
 Db 1975 TGGGAATATATGACGCTATCGCAGAAAAAGATTTTCAAGATGTTATGGATCAAAATC--- 2031
 QY 373 GluLeuAspSerAlaSerArgTyrProValLeu---ThrAlaLeuLeuLeuTyrArgLys 391
 Db 2032 AAGTATTATGATTTGAACACACAAACATCATAGAAATTAGCAGACGATATATATGAA 2091
 QY 392 IleLeuAspGluIleGluAlaAsnAspTyrAsnAsnPheThrArgArgAlaTyrValSer 411
 Db 2092 ATACTGGACGAGTGAAGCAGCGCTAACTAT---ACATTACATGACGCTGTTTGGGAT 2148
 QY 412 LysProLysLys 415
 Db 2149 AAGAGAAAAAG 2160

RESULT 15

US-09-738-626-695
 ; Sequence 695, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: Patent in ver. 3.0
 ; SEQ ID NO 695
 ; LENGTH: 912
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-695

Alignment Scores:

Pred. No.:	9,95e-16	Length:	912
Score:	204.00	Matches:	87
Percent Similarity:	41.45%	Conservative:	39
Best Local Similarity:	28.62%	Mismatches:	130
Query Match:	8.99%	Indels:	48
DB:	9	Gaps:	11

US-09-847-081b-2 (1-440) x US-09-738-626-695 (1-912)
 QY 147 TyrAspArgCysGly-----GluValCysAlaGluTyrAlaLysThrPhe 161
 Db 49 TACAATCGGCGCTCATTCAGGCTTCACATAAAGTCATGAAGAATATTCGACGAGCTTC 108
 QY 162 TyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrPheAlaIleThrVal 181
 Db 109 ATCTGTCTACCTGGTGTCTATCCCGCCGATACGAAATGACATACGAAATCTCTATGCA 168
 QY 182 TrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln 201
 Db 169 GTAGTTCGTATCCCGATGAGTTGTCAGCGC-----ACTGCACAT 210
 QY 202 AlaLeuAspArgTyrProGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMet 221
 Db 211 GCCCTGGTGTCTCAACTGCCAAAATCGAAGAGATTTCTCGATCCCTATGAAATTCGGT 270
 QY 222 LeuAspAla-----AlaLeuSerAspThr 229
 Db 271 CTGCGACGCCACCAACACGCTTCAACACAGATCTTGTGTTTACAGCTTATGTTGAAC 330
 QY 230 ValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMetArgMet 249
 Db 331 GCCCGACGCTGTCATTTCCAAACAGAGCATGTAATAGCCTTCTTTCATCATCAATCGCTA 390
 QY 250 AspLeuTyrPheSerArgTyrLysThrPheAspGluLeuTyrLysTyrCysTyrThrVal 269
 Db 391 GACCTC---AAAGCTAATACACAGCACCAGATAGTTCACACAGTATGCTATGGCTCC 447
 QY 270 AlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGlu---SerLys 288
 Db 448 GCGGAAGTTATAGGCTGCTTGTCTCAGCGTTTTCACCAAGTAGAAGATAGCAAA 507
 QY 289 AlaThrThrGluSerValTyrAsnAlaAlaLeuAlaGlyLeuAlaAsnGlnLeuThr 308
 Db 508 AACCGCTAGAGATTATGCAAAACGGAGCGCTCATTTGGGAGCGGATTCACAGAAAT 567
 QY 309 AsnIleLeuArgAspValGlyGluAspAlaArgArg---GlyArgValTyrLeuProGln 327
 Db 568 AACTTCTCCGTGACTTGGCAGAAGATCAGCAAAATTTGGGCGGATTTTATTTCCCGC--- 624
 QY 328 AspGluLeuAlaGlnAlaGlyLeuSer-----AspGluAspIlePheAlaGlyArg 344
 Db 625 ---AAACCCAGCAAGGAATCTTACTAAGAACAAAGAAAGATCTCATCGCTGAT--- 678
 QY 345 ValThrAspLysTyrArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePhe 364
 Db 679 -----ATCCGTCAGACCTAGCAATTCGCCACGATGCATTT 714
 QY 365 AspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTyrProValLeuThr 384
 Db 715 -----CCAGAAATACCAAGTCAGCTCGCATCGGAGTGATCTCT 753
 QY 385 AlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsnAsnPhe 404
 Db 754 GCTTATTTGCTCTTTCAAAACACTACTACCGCAATTTGAGGCTACTCTACCGCGCGG 813
 QY 405 ThrArg---ArgAlaTyrValSerLysProLysLysLeuThrLeuProIleAlaTyr 423
 Db 814 TTGCGGGAGCGAATCAGAGTTCCACTTCATATCAAACTCTCTACACTCGGTAGGCGACG 873
 QY 424 AlaLysSerLeu 427
 Db 874 ATGAAAGGTCTA 885

Search completed: April 5, 2003, 05:21:58
 Job time : 306 secs